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Figure 1a

1 MALPNKFFLW FCCFAWLCFP ISLDSLPSRG EAQIVARTAL ESEAETWSLL

R87H [E1]



51 NHLGGRHRPG LLSPLLEVLY DGHGEPRLQ PDDRALRYMK RLYKAYATKE



101 GTPKSNRRHL YNTVRLFTPC AQHKQAPGDL AAGTFPSVDL LFNLDRTTVV

151 EHLFKSVLLY TFNNSISFPF PVKCICNLVI KEPEFSSKTL PRAPYSFTYN

E241K [324]



201 SQFEFRKKYK WMEIDVTAPL EPLVASHKRN IHMSVNFTCA EDQLQHPSAR

251 DSLENMTLLV APSLLLYLND TSAQAFHRWH SLHPKRKPSQ GPDQKRGLSA

(I)

V332I [597]



301 YPVGEEAAEG VRSS[REDACTED]DQ ESASSELKKP LVPASVNLSE YFKQFLFPQN

V371M [714]



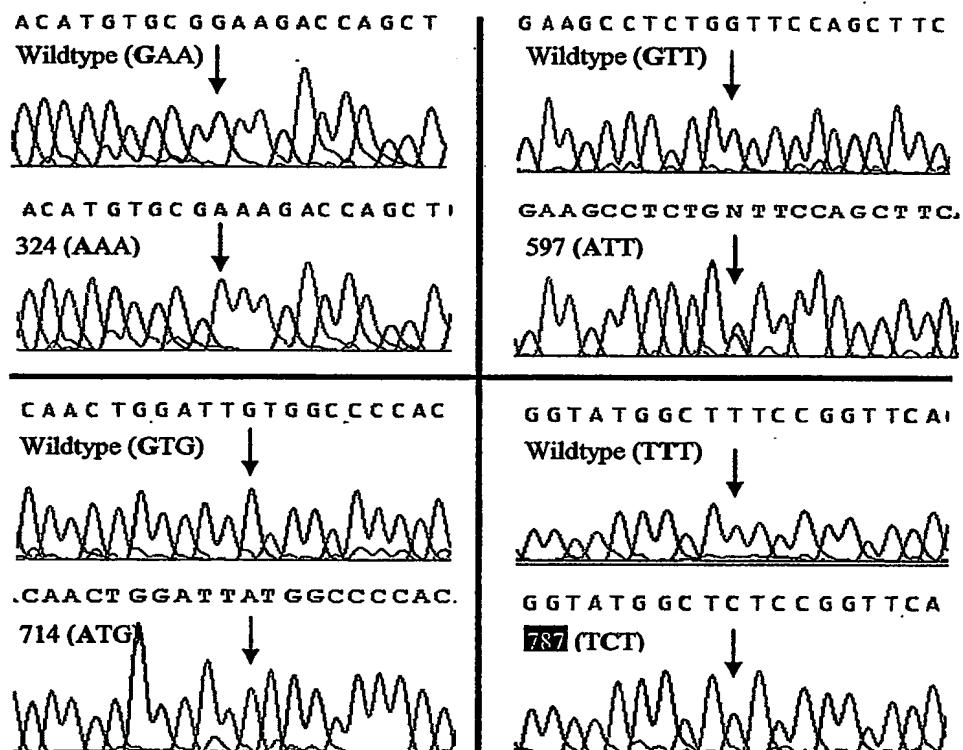
S395F [787]

351 ECELHDFRLS FSQKWDNWI VAPHKYNPRY CKGDCPRAVG HRYG[REDACTED]PVHTM

401 VQNIIEKLD SSVPRPSCVP AKYSPLSVLA IEPDGSIAYK EYEDMIATKC

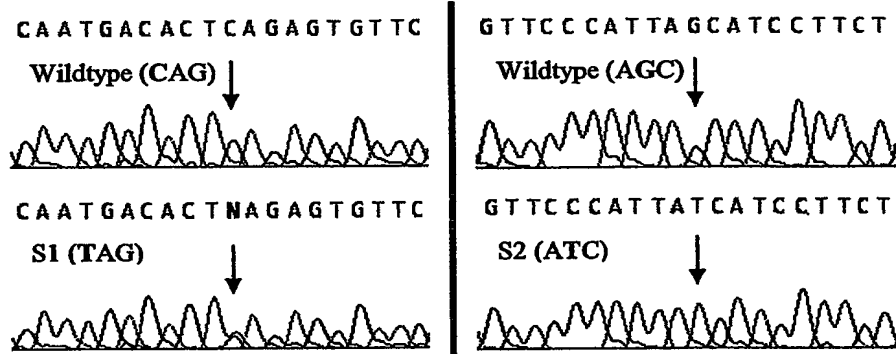
(135)

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Figure 1b

1 MVLLSILRIL LWGLVLFMEH RVQMTQVGQP SIAHLPEAPT LPLIQELLE
51 APGKQQRKPR VLGHPLRYML ELYQRSADAS GHPRENRTIG ATMVRLVRPL
101 ASVARPLRGS WHIQTLDFPL RPNRVAYQLV RATVVYRHQL HLTHSHLSCH
151 VEPWVQKSPT NHFPSSGRGS SKPSLLPKTW TEMDIMEHVG QKLWNHKGRR
201 VLRLRFVCQQ PRGSEVLEFW WHGTSSLDTV FLLLYFNDTQ SVQKTKPLPK
251 GLKEFTEKDP SLLLQQA GSIASEVPGP SREHDGPESN QCSLHPFQVS
301 FQQLGWDHWI IAPHLYTPNY CKGVCPRVLH YGLNSPNHAI IQNLVSELVD
351 QNVPPQSCVP YKYVPISILL IEANGSILYK EYEGMIAQSC TCR

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Figure 2b

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Figure 3a

Animal		R 8 3 0	9 3 0 4 5 8	9 3 0 4 5 9	9 7 0 4	9 3 0 8 1 1	9 3 0 8 1 2	8 7 8 3	9 3 0 8 1 0	9 4 8 3 0 2	7 8 1 0
Phenotype Sterile (S) Fertile (F)		n/a	S	S	F	S	S	F	F	F	F
G E N O T Y P E	S1	+/Y	S1/+	S1/+	S1/+	+/+	+/+	+/+	+/+	+/+	+/+
	S2	S2/Y	S2/+	S2/+	+/+	S2/+	S2/+	+/+	S2/+	S2/+	+/+
	787	T/+	T/+	+/+	+/+	T/T	T/T	T/+	+/+	+/+	+/+

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Figure 3b

Animal		9 6 2 1 0 1	9 9 7 6 3 4	9 9 7 6 3 5	9 6 2 1 5 2	9 9 7 5 5 2	9 9 7 5 5 3	9 7 6 2 3 4	9 3 0 1 4 2	9 4 8 0 9 3	8 8 7 4
Phenotype Sterile (S) Fertile (F)		n/a	S	S	F	F	S	F	n/a	S	F
G E N O T Y P E	S1	S1/Y	S1/S1	S1/S1	S1/+	S1/+	S1/S1	S1/+	S1/Y	S1/+	+/+
	S2	+/Y	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+
	787	T/+	T/T	T/T	T/+	T/+	T/+	+/+	T/T	T/T	T/+

atg	gcg	ctt	ccc	aac	aaa	ttc	ttc	ctt	tgg	ttt	tgc	tgc	ttt	gcc
Met	Ala	Leu	Pro	Asn	Lys	Phe	Phe	Leu	Trp	Phe	Cys	Cys	Phe	Ala
		-315						-310					-305	
tgg	ctc	tgt	ttt	cct	att	agc	ctt	gat	tct	ctg	cct	tct	agg	gga
Trp	Leu	Cys	Phe	Pro	Ile	Ser	Leu	Asp	Ser	Leu	Pro	Ser	Arg	Gly
		-300						-295					-290	
gaa	gct	cag	att	gta	gct	agg	act	gcg	ttg	gaa	tct	gag	gct	gag
Glu	Ala	Gln	Ile	Val	Ala	Arg	Thr	Ala	Leu	Glu	Ser	Glu	Ala	Glu
		-285						-280					-275	
act	tgg	tcc	ttg	ctg	aac	cat	tta	ggg	ggg	aga	cac	aga	cct	ggg
Thr	Trp	Ser	Leu	Leu	Asn	His	Leu	Gly	Gly	Arg	His	Arg	Pro	Gly
		-270						-265					-260	
ctc	ctt	tcc	cct	ctc	tta	gag	gtt	ctg	tat	gat	ggg	cac	ggg	gaa
Leu	Leu	Ser	Pro	Leu	Leu	Glu	Val	Leu	Tyr	Asp	Gly	His	Gly	Glu
		-255						-250					-245	
									[E1]					
ccc	ccc	agg	ctg	cag	cca	gat	gac	aga	gct	ttg	cgc	tac	atg	aag
Pro	Pro	Arg	Leu	Gln	Pro	Asp	Asp	Arg	Ala	Leu	Arg	Tyr	Met	Lys
		-240						-235					-230	
agg	ctc	tat	aag	gca	tac	gct	acc	aag	gag	ggg	acc	cct	aaa	tcc
Arg	Leu	Tyr	Lys	Ala	Tyr	Ala	Thr	Lys	Glu	Gly	Thr	Pro	Lys	Ser
		-225						-220					-215	
aac	aga	cg	cac	ctc	tac	aac	act	gtt	cgg	ctc	ttc	acc	ccc	tgt
Asn	Arg	Arg	His	Leu	Tyr	Asn	Thr	Val	Arg	Leu	Phe	Thr	Pro	Cys
		-210						-205					-200	
									Intron position					
gct	cag	cac	aag	cag	gct	cct	ggg	gac	ctg	gcg	gca	g	ga	acc
Ala	Gln	His	Lys	Gln	Ala	Pro	Gly	Asp	Leu	Ala	Ala	G	gly	Thr
		-195						-190					-185	
cca	tca	gtg	gat	ctg	ctg	ttt	aac	ctg	gat	cgt	gtt	act	gtt	gtg
Pro	Ser	Val	Asp	Leu	Leu	Phe	Asn	Leu	Asp	Arg	Val	Thr	Val	Val
		-180						-175					-170	
									[74]					
gaa	cat	tta	ttc	aag	tca	gtg	ttg	ctg	tat	act	ttc	aac	aac	tcc
Glu	His	Leu	Phe	Lys	Ser	Val	Leu	Leu	Tyr	Thr	Phe	Asn	Asn	Ser
		-165						-160					-155	
att	tct	ttt	ccc	ttt	cct	gtt	aaa	tgt	ata	tgc	aac	ctg	gtg	ata
Ile	Ser	Phe	Pro	Phe	Pro	Val	Lys	Cys	Ile	Cys	Asn	Leu	Val	Ile
		-150						-145					-140	
aaa	gag	cca	gag	ttt	tct	agc	aag	act	ctc	cct	aga	gct	cca	tac
Lys	Glu	Pro	Glu	Phe	Ser	Ser	Lys	Thr	Leu	Pro	Arg	Ala	Pro	Tyr
		-135						-130					-125	
tca	ttt	acc	tat	aac	tca	cag	ttt	gaa	ttt	aga	aag	aaa	tac	aaa
Ser	Phe	Thr	Tyr	Asn	Ser	Gln	Phe	Glu	Phe	Arg	Lys	Lys	Tyr	Lys
		-120						-115					-110	

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Figure 4 continued

cac aag agg aat att cac atg tct gta aat ttt aca tgt gcg <u>gaa</u> gac	726
His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala <u>Glu</u> Asp	
-90 -85 -80	
cag ctg cag cat cct tca gcg cgg gac agc ctg ttt aac atg act ctt	774
Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu	
-75 -70 -65	
ctc gta gcg ccc tca ctg ctt ttg tat ctg aac gac aca agt gct cag	822
Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln	
-60 -55 -50 -45	
gct ttt cac agg tgg cat tcc ctc cac cct aaa agg aag cct tca cag	870
Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln	
-40 -35 -30	
ggt cct gac cag aag aga ggg cta tct gcc tac ccc gtg gga gaa gaa	918
Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu	
-25 -20 -15	
gct gct gag ggt gta aga tcg tcc cgt cac cgc aga gac cag gag agt	966
Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser	
-10 -5 -1 1	
[581] [597]	
gcc agc tct <u>gaa</u> ttg aag aag cct ctg <u>gtt</u> cca gct tca gtc aat ctg	1014
Ala Ser Ser Glu Leu Lys Lys Pro Leu <u>Val</u> Pro Ala Ser Val Asn Leu	
5 10 15 20	
agt gaa tac ttc aaa cag ttt ctt ttt ccc cag aat gaa tgt gag ctc	1062
Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu	
25 30 35	
cat gac ttt aga ctt agc ttt agt cag ctg aag tgg gac aac tgg att	1110
His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile	
40 45 50	
[714]	
<u>gtg</u> gcc cca cac aaa tac aac cct cga tac tgt aaa ggg gac tgt ccc	1158
<u>Val</u> Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro	
55 60 65	
[787]	
agg gcg gtc gga cat cgg tat ggc <u>tgt</u> ccg gtt cac acc atg gtg cag	1206
Arg Ala Val Gly His Arg Tyr Gly <u>Ser</u> Pro Val His Thr Met Val Gln	
70 75 80	
aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga cca tcc tgt	1254
Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys	
85 90 95 100	
gta cct gcc aag tat agc cct ttg agt gtt ttg gcc atc gag cct gat	1302
Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp	
105 110 115	
ggc tca atc gct tat aaa gaa tat gaa gat atg ata gcc act aag tgt	1350
Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys	
120 125 130	
acc tgt cgt taa cagactc ctgtcaagta aaacatgag tgtcctggcc	1399
Thr Cys Arg STOP	
135	
agtgtaaatg ccgcgcc	1416

Figure 5

.atg gtc ctc ctg agc atc ctt aga atc	27
.Met Val Leu Leu Ser Ile Leu Arg Ile	-265 -260
[Leu] deletion		
<u>ctt</u> ctt tgg gga ctg gtg ctt ttt atg gaa cat agg gtc caa atg	72	
<u>Leu</u> Leu Trp Gly Leu Val Leu Phe Met Glu His Arg Val Gln Met	-255 -250 -245	
aca cag gta ggg cag ccc tct att gcc cac ctg cct gag gcc cct	117	
Thr Gln Val Gly Gln Pro Ser Ile Ala His Leu Pro Glu Ala Pro	-240 -235 -230	
acc ttg ccc ctg att cag gag ctg cta gaa gaa gcc cct ggc aag	162	
Thr Leu Pro Leu Ile Gln Glu Leu Leu Glu Glu Ala Pro Gly Lys	-225 -220 -215	
cag cag agg aag ccg cgg gtc tta ggg cat ccc tta cgg tat atg	207	
Gln Gln Arg Lys Pro Arg Val Leu Gly His Pro Leu Arg Tyr Met	-210 -205 -200	
ctg gag ctg tac cag cgt tca gct gac gca agt gga cac cct agg	252	
Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser Gly His Pro Arg	-195 -190 -185	
gaa aac cgc acc att ggg gcc acc atg gtg agg ctg gtg agg ccg	297	
Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu Val Arg Pro	-180 -175 -170	
Intron position		
ctg gct agt gta gca agg cct ctc aga g-----gc	327	
Leu Ala Ser Val Ala Arg Pro Leu Arg Gly	-165 -160	
tcc tgg cac ata cag acc ctg gac ttt cct ctg aga cca aac ccg	372	
Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg	-155 -150 -145	
gta gca tac caa cta gtc aga gcc act gtg gtt tac cgc cat cag	417	
Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val Tyr Arg His Gln	-140 -135 -130	
ctt cac cta act cat tcc cac ctc tcc tgc cat gtg gag ccc tgg	462	
Leu His Leu Thr His Ser His Leu Ser Cys His Val Glu Pro Trp	-125 -120 -115	
gtc cag aaa agc cca acc aat cac ttt cct tct tca gga aga ggc	507	
Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser Ser Gly Arg Gly	-110 -105 -100	
tcc tca aag cct toc ctg ttg ccc aaa act tgg aca gag atg gat atc	555	
Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp Ile	-95 -90 -85	
atg gaa cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg gtt	603	
Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Val	-80 -75 -70	

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Figure 5 continued

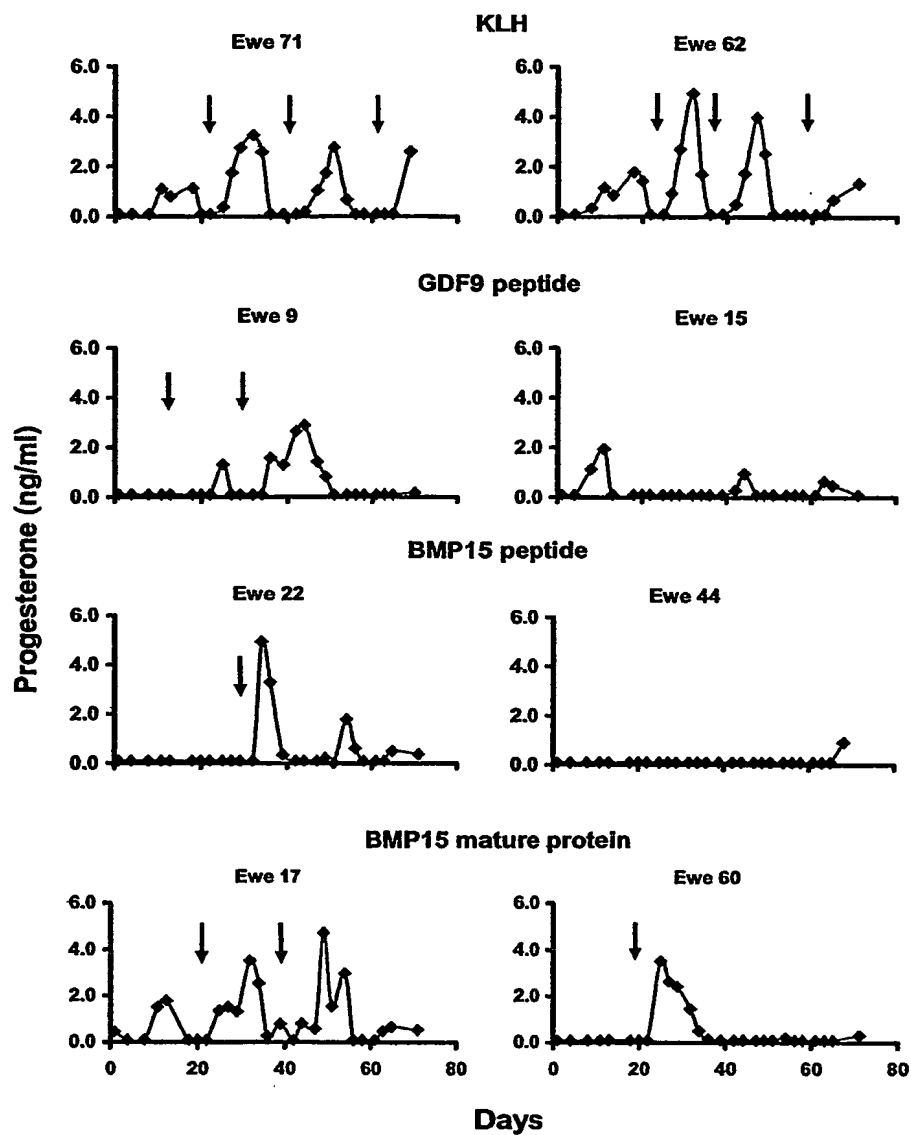
cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt	651
Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val Leu	
-65 -60 -55	
 gag ttc tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta	699
Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu Leu	
-50 -45 -40	
 [S1] [422]	
ctg tat ttc aat gac act cag agt gtt cag aag acc aaa cct ctc cct	747
Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr Lys Pro Leu Pro	
-35 -30 -25 -20	
 aaa ggc ctg aaa gag ttt aca gaa aaa gac cct tct ctt ctc ttg agg	795
Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Leu Leu Leu Arg	
-15 -10 -5	
 agg gct cgt caa gca ggc agt att gca tgc gaa gtt cct ggc ccc tcc	843
Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val Pro Gly Pro Ser	
-1 1 5 10	
 agg gag cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt	891
Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe	
15 20 *** 25	
 caa gtc agc ttc cag cag ctg ggc tgg gat cac tgg atc att gct ccc	939
Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro	
30 *** 35 40 45	
 cat ctc tat acc cca aac tac tgt aag gga gta tgt cct cgg gta cta	987
His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys Pro Arg Val Leu	
50 55 60	
 cac tat ggt ctc aat tct ccc aat cat gcc atc atc cag aac ctt gtc	1035
His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile Gln Asn Leu Val	
65 70 75	
 agt gag ctg gtg gat cag aat gtc cct cag cct tcc tgt gtc cct tat	1083
Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr	
80 85 90	
 [S2]	
aag tat gtt ccc att agc atc ctt ctg att gag gca aat ggg agt atc	1131
Lys Tyr Val Pro Ile Ser Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile	
95 100 105	
 ttg tac aag gag tat gag ggt atg att gcc cag tcc tgc aca tgc agg	1179
Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser Cys Thr Cys Arg	
110 115 120 125	
 tga cggcaaagggtgca	
STOP	

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Figure 6

BMP2 Human	QAKHKQRKRLKS-----SKRHPLYVDFS-DVGWND
BMP7/OP1 Human	STGSKQRSQNRSKTPKNQEARLMAENSSSDQROAKKHELYVSFR-DLGWQD
GDF9 SHEEP	RDQESASSELKKPLVPASVNLSEYFKQFLFP---QNEELHDFRLSFS-QLKWDN
GDF9 Human	GOETVSSELKKPLGPASVNLSEYFRQFLLP---QNEELHDFRLSFS-QLKWDN
GDF9 Mouse	GQKAIRSEAKGPLLTASVNLSEYFKQFLFP---QNEELHDFRLSFS-QLKWDN
GDF9B SHEEP	QAGSIASEVPGPSREHDGPE-----SNQSLHFPQVSFQ-QLGWDH
GDF9B Mouse	QACSIESDASCPSQEHGDSV-----NNQSLHYPKVSFH-QLGWDH
GDF9B Human	QADGISAETASSSKHSGPE-----NNQSLHFPQISFR-QLGWDH
TGFB2 Human	ALDAAYCFRNVQDN-----CLRPLYIDFKRDLGWK-
TGFB3 Human	ALDTNYCFRNLEEN-----CVRPLYIDFRQDLGWK-
TGFB1 Human	ALDTNYCFSSTEKN-----CVRQLYIDFRKDLGWK-
	0 10 20 30 40 50
BMP2 Human	WIVAPPGYHAFYHGEPPFLADHLNSTNHAI VQTLVNSVN-SKIPKAVPTELSAISM
BMP7/OP1 Human	WIIAPEGYAAAYEGERAFPLNSYMNATNHAI VQTLVHFINPETVPKPAPTQLNAISV
GDF9 SHEEP	WIVAPHKYNPRYKGDPRAVGHRYGSPVHTMVQNI IHEKLDSSVPRPSVPAKYSPLSV
GDF9 Human	WIVAPHRYNPRYKGDPRAVGHRYGSPVHTMVQNI IYEKLDSSVPRPSVPAKYSPLSV
GDF9 Mouse	WIVAPHRYNPRYKGDPRAVRHRYGSPVHTMVQNI IYEKLDPSVPRPSVPGKYSPLSV
GDF9B SHEEP	WIIAPHLTYTPNYKGVSPRVLYGLNSPNHAI IQNLVSELVDQNVQPSVVPKYVPISTI
GDF9B Mouse	WIIAPRLTYTPNYKGIITRVLPYGLNSPNHAI IQSLVNELVNHVSVPQPSVPYNFLPMSI
GDF9B Human	WIIAPPFYTPNYKGTLRVLRDGLNSPNHAI IQNLINQLVDQSVPRPSVVPKYVPISV
TGFB2 Human	WIHEPKGYNANFAGAPYLWS---SDTQHSRVLSLYNTINPEASASPVSDLEPLTI
TGFB3 Human	WVHEPKGYANFSGPPYLRS---ADTTHSTVLGLYNTLNPEASASPVQDLEPLTI
TGFB1 Human	WIHEPKGYHANFELGPPYIWS---LDTQYSKVLALYNQHNPGASAAPVPOALEPLPI
	60 70 80 90 100 * 110
BMP2 Human	LYLDENEKVVLKNYQDMVVEGGER
BMP7/OP1 Human	LYFDDSSNVILKKYRNMVVRAAGH
GDF9 SHEEP	LAIEPDGSIAYKEYEDMIATKTER
GDF9 Human	LTIEPDGSIAYKEYEDMIATKTER
GDF9 Mouse	LTIEPDGSIAYKEYEDMIATRTER
GDF9B SHEEP	LLIEANGSILYKEYEGMIAQSETER
GDF9B Mouse	LLIETNGSILYKEYEGMIAQSETER
GDF9B Human	LMIEANGSILYKEYEGMIAESETER
TGFB2 Human	LYYIGK-TPKIEQLSNMIVKSSEKES
TGFB3 Human	LYYVGR-TPKVEQLSNMVVKSSEKES
TGFB1 Human	VYYVGR-KPKVEQLSNMIVRSSEKES
	120 130 140

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Figure 7

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Figure 8